#### SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: Bryan, Bruce
- (ii) TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Heller Ehrman White & McAuliffe
  - (B) STREET: 4250 Executive Square, 7th Floor
  - (C) CITY: La Jolla
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/757,046
  - (B) FILING DATE: 11-25-96 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/597,274
  - (B) FILING DATE: 02-06-96
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Seidman, Stephanie L
  - (B) REGISTRATION NUMBER: 33,779
  - (C) REFERENCE/DOCKET NUMBER: 24727-105C
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 619-450-8400
  - (B) TELEFAX: 619-450-8499 (C) TELEX:

  - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1196 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...942





# (D) OTHER INFORMATION: Renilla Reinformis Luciferase

# (x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

			ATG Met														48
			GGT Gly 20													:	96
			TTT Phe													1	44
			TTT Phe													1	92
			CCA Pro													2	40
			ATG Met													2	88
			CAT His 100													3:	36
			AGA Arg													3	84
			TAT Tyr													4:	32
			AGT Ser													4	80
			GAA Glu													5:	28
			GAG Glu 180													5	76
			AAG Lys													6:	24
			AAA Lys													6'	72
GAA	ATC	CCG	TTA	GTA	AAA	GGT	GGT	AAA	CCT	GAC	GTT	GTA	CAA	ATT	GTT	7:	20

Glu 225	Ile	Pro	Leu	Val	Lys 230	Gly	Gly	Lys	Pro	Asp 235	Val	Val	Gln	Ile	Val 240	
											GAT Asp					768
											GCT Ala					816
											GTA Val					864
											AAA Lys 300					912
	GTT Val									TAA	TTAC	CTTTC	GT :	TTTT	TATTTA	965
TTTC ATTI	CACAC	GG A	ACAT ATTAC	TCAT	TA TA	ATGTT CAATO	GATT SAAAC	AAT	ATT?	ACA	GAAC	CTTTA STTCA	ACT (	CTGT(	TGAATA CATATC TAATAT	1025 1085 1145 1196

#### (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1822 base pairs (B) TYPE: nucleic acid

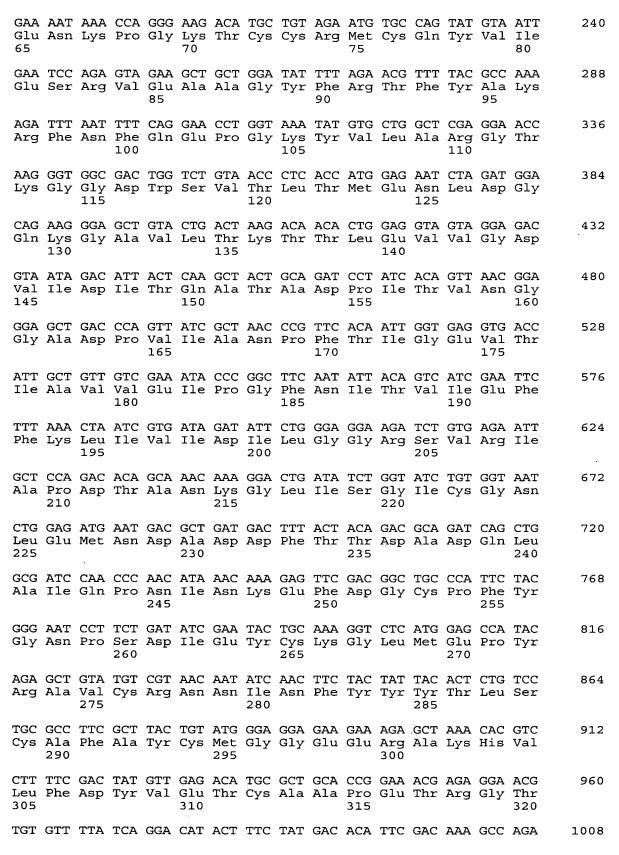
  - (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...1665

  - (D) OTHER INFORMATION: Cypridina hilgendorfii luciferase
- (x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

 			 		 	GTC Val		48
 	 	 	 	 	 	 TCA Ser 30	 	96
 	 	 	 	 	 	 TGT Cys	 	144
 	 	 	 	 	 	 GGA Gly	 	192



Cys	Val	Leu	Ser	Gly 325	His	Thr	Phe	Tyr	Asp 330	Thr	Phe	Asp	Lys	Ala 335	Arg	
	CAA Gln															1056
	TGG Trp															1104
	ACT Thr 370															1152
	TTG Leu															1200
	ATC Ile															1248
	ATC Ile															1296
	TTT Phe														GGA Gly	1344
	ACA Thr 450															1392
	TTT Phe															1440
	ACA Thr															1488
	GAT Asp															1536
	ATT Ile															1584
	TGT Cys 530															1632
	GAC Asp										TAA	ATGA	AACAA	AAG		1678
	CTTAT	CT GA	ATGT	ACTCA	TTC	TTT									AAAC TAACG	1738 1798 1822

(2) INFORMATION FOR SEQ ID NO:3:

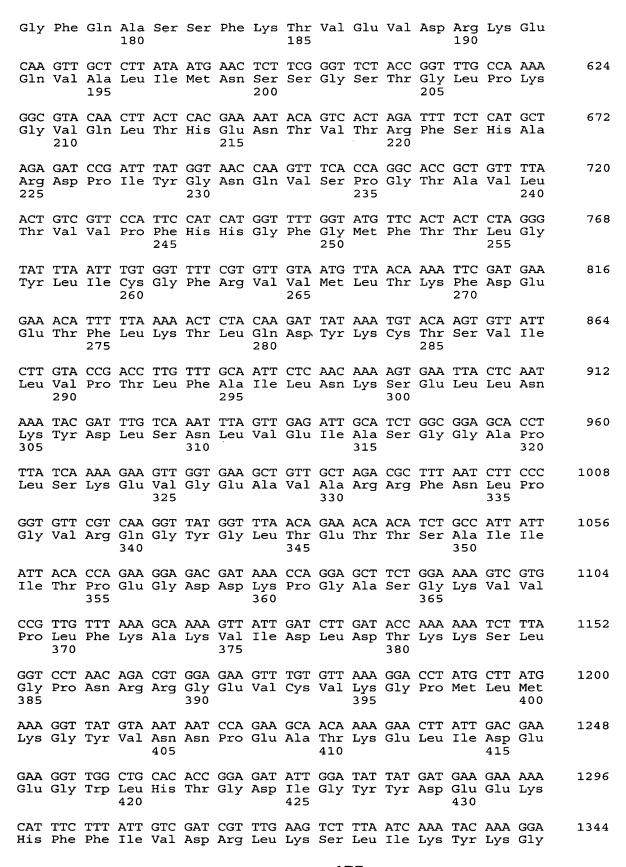
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1644 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence

  - (B) LOCATION: 1...1644
    (D) OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)
- (x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

					AAC Asn											48
					GAG Glu											96
_					AAA Lys											144
					TCT Ser											192
					CAA Gln 70											240
					AAC Asn			_								288
					GTA Val		-									336
					CAC His											384
					GGC Gly											432
					ACC Thr 150											480
					CTG Leu											528
GGT	TTT	CAA	GCA	TCC	AGT	TTC	AAA	ACT	GTG	GAA	GTT	GAC	CGT	AAA	GAA	576



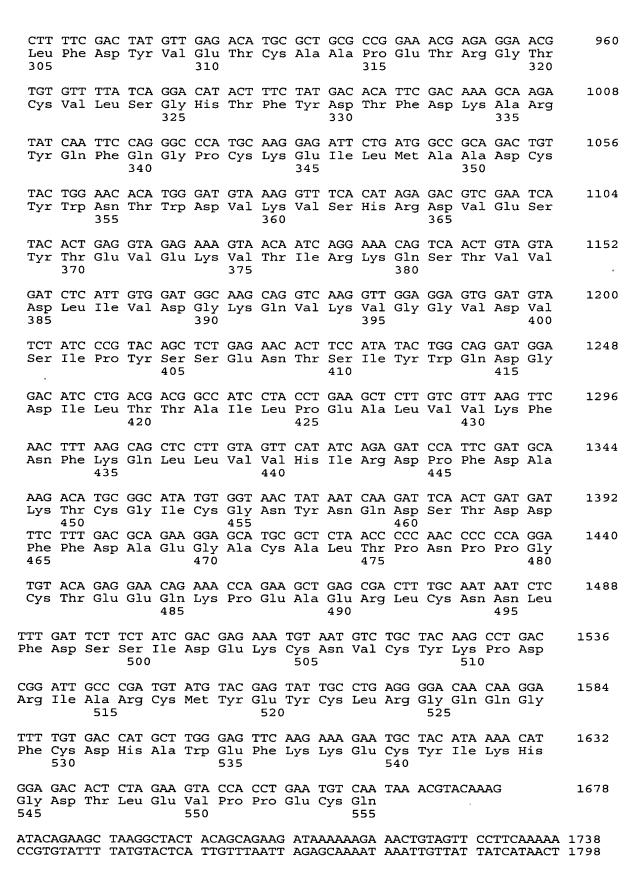
435 440 445 TAC CAA GTA CCA CCT GCC GAA TTA GAA TCC GTT CTT TTG CAA CAT CCA 1392 Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro 455 450 TCT ATC TTT GAT GCT GGT GTT GCC GGC GTT CCT GAT CCT GTA GCT GGC 1440 Ser Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Val Ala Gly 470 475 GAG CTT CCA GGA GCC GTT GTT GTA CTG GAA AGC GGA AAA AAT ATG ACC 1488 Glu Leu Pro GLy Ala Val Val Leu Glu Ser Gly Lys Asn Met Thr 485 490 GAA AAA GAA GTA ATG GAT TAT GTT GCA AGT CAA GTT TCA AAT GCA AAA 1536 Glu Lys Glu Val Met Asp Tyr Val Als Ser Gln Val Ser Asn Ala Lys 500 CGT TTA CGT GGT GGT GTT CGT TTT GTG GAT GAA GTA CCT AAA GGT CTT 1584 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu 515 520 ACT GGA AAA ATT GAC GGC AGA GCA ATT AGA GAA ATC CTT AAG AAA CCA 1632 Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro 530 535 GTT GCT AAG ATG 1644 Val Ala Lys Met 545

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1820 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...1664
  - (D) OTHER INFORMATION: Vargula (cypridina) luciferase
- (x) PUBLICATION INFORMATION:
  - JP 3-30678 Osaka (Tsuji)
  - (A) AUTHORS: Thompson <u>et al.</u>
    (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
  - (D) VOLUME: 86
  - (F) PAGES: 1326-1332
  - (G) DATE: (1989)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

					TTG Leu 10				48	3
	 	 	 	 	GCG Ala	 	 	 	96	5

25 20 CCA ACA GTT CCA ACT TCT TGT GAA GCT AAA GAA GGA GAA TGT ATA GAT 144 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp

	35			40			45			
			TGT Cys						1	192
			AAG Lys 70						2	240
			GCA Ala						2	288
			GAA Glu						3	336
			TCT Ser						3	384
			CTG Leu						4	432
			CAA Gln 150						4	180
			ATC Ile						5	528
			ATA Ile						5	576
			ATT Ile						6	524
			AAC Asn						6	572
			GCT Ala 230						7	720
			ATA Ile						7	768
			ATC Ile						8	316
			AAC Asn						8	364
			TGT Cys						9	912



## ТАААСТАААА ААААААААА АА

1820

#### (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 958 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
  (ix) FEATURE:
- - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 115...702
  - (D) OTHER INFORMATION: apoaequorin-encoding gene
- (x) PUBLICATION INFORMATION:

PATENT NO.: 5,093,240

- (A) AUTHORS: Inouye et al.
  (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
  (D) VOLUME: 82
- (F) PAGES: 3154-3158
- (G) DATE: (1985)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGGGGGGG GGG	GGGGGGG GGGGG	GGGGG GGGAATGCAA	TTCATCTTTG CATC	AAAGAA 60
TTACATCAAA TCT	CTAGTTG ATCAA	CTAAA TTGTCTCGAC	AACAACAAGC AAAC	ATG 117 Met 1
	n Tyr Ser Val	AAG CTT ACA TCA Lys Leu Thr Ser 10		
		CAT ATG TTC AAT His Met Phe Asn 25	_	
		GAC GAG ATG GTC Asp Glu Met Val	_	
		GCA ACA CCT GAG Ala Thr Pro Glu 60		
		TTC GGA GGA GCT Phe Gly Gly Ala 75		
	p Trp Pro Ala	TAT ATT GAA GGA Tyr Ile Glu Gly 90		
		GCC AAA AAC GAA Ala Lys Asn Glu 105		

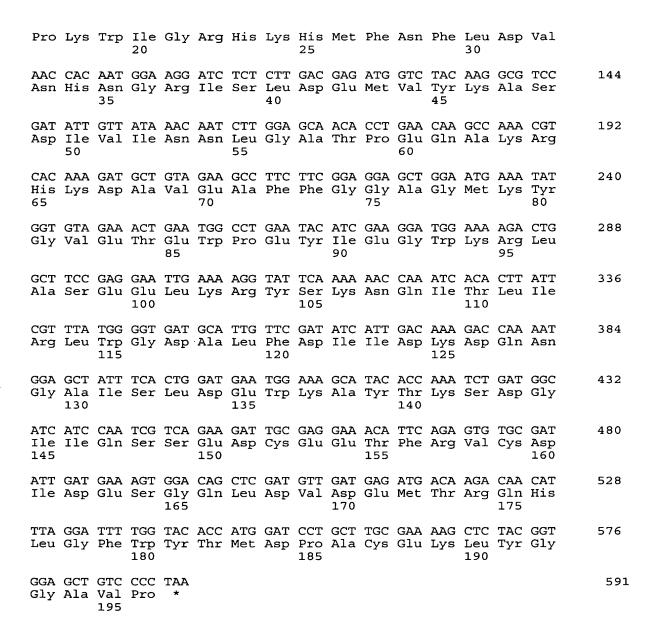
														AAT Asn		501
														GGT Gly		549
														GAT Asp 160		597
														CAT His		645
														GGT Gly		693
	GTC Val 195		TAAC	SAAGO	TC I	CACGO	TGGT	G A	ATGCA	CCCI	CA GO	BAAGA	ATGAT	r GTG	SATTTTGA	752
TGTT AGAA	GATT CTTA	TT I	GTAZ	TTAC	G AA	CAGA	ATTA AAAA	ATC	GAAT	GAT	TAGI	TGTT	TT T	TTAF	CGTTTG ATCAAC AAAAAA	812 872 932 958

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 591 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...588
  - (D) OTHER INFORMATION: Recombinant Aequorin AEQ1
- (x) PUBLICATION INFORMATION:
  - (A) AUTHORS: Prasher et al.
  - (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
  - (C) JOURNAL: Biochemistry
  - (D) VOLUME: 26
  - (F) PAGES: 1326-1332
  - (G) DATE: 1987
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

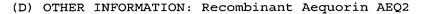
ATG	ACC	AGC	GAA	CAA	TAC	TCA	GTC	AAG	CTT	ACA	CCA	GAC	TTC	GAC	AAC	48
Met	Thr	Ser	Glu	Gln	Tyr	Ser	Val	Lys	Leu	Thr	Pro	Asp	Phe	Asp	Asn	
1				5					10					15		

CCA AAA TGG ATT GGA CGA CAC AAG CAC ATG TTT AAT TTT CTT GAT GTC 96



## (2) INFORMATION FOR SEQ ID NO:7:

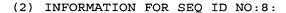
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 591 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...588



- (x) PUBLICATION INFORMATION:
- (A) AUTHORS: Prasher et al.(B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
- (C) JOURNAL: Biochemistry
  (D) VOLUME: 26
  (F) PAGES: 1326-1332

- (G) DATE: 1987
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC Thr											48
AGA Arg									_		96
CAC His										1	144
ATT Ile 50							_	_		1	.92
AAA Lys							_			2	240
GTG Val										2	88
ACT Thr										3	336
 ATA Ile	 	-								3	884
GCC Ala 130										4	132
ATC Ile										4	180
GAT Asp										5	528
GGA Gly					_	_			_	5	576
GCT Ala		TAA *									591



- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 591 base pairs (B) TYPE: nucleic acid

  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...588
  - (D) OTHER INFORMATION: Recombinant Aequorin AEQ3

#### (x) PUBLICATION INFORMATION:

- (A) AUTHORS: Prasher et al.
- (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
- (C) JOURNAL: Biochemistry (D) VOLUME: 26
- (F) PAGES: 1326-1332
- (G) DATE: 1987

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

		TAC Tyr						48
		CGA Arg						96
		ATC Ile						144
		AAC Asn						192
		GGA Gly 70						240
		TGG Trp						288
		GAG Glu						336
		GCT Ala						384
		GAT Asp						432

	130								140					
_	ATC Ile	-	_	_			 	 	Phe				_	480
	GAT Asp													528
	GGA Gly													576
	GCT Ala													591

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 567 base pairs

  - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...567
  - (D) OTHER INFORMATION: Aequorin photoprotein

#### (x) PUBLICATION INFORMATION:

- (A) AUTHORS: Charbonneau et al.
- (B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin
- (C) JOURNAL: Am. Chem. Soc. (D) VOLUME: 24
- (E) ISSUE: 24
- (F) PAGES: 6762-6771
- (G) DATE: 1985

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

			GAC Asp						48
			TTT Phe					 	96
		_	 TAC Tyr	 	 	 	 	 	144
			CAA Gln		 		 	 	192

50			55						60						
TTC Phe													240		
TAC Tyr													288		
TCA Ser	-												336		
GAT Asp												GAA Glu	384		
 AAA Lys 130	 _		_										432		
GAG Glu													480		
GTT Val													528		
CCT Pro													567		

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 588 base pairs
  - (B) TYPE: nucleic acid(C) STRANDEDNESS: single

  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...588
- (D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activity
  - (x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

- (K) RELEVANT RESIDUES IN SEQ ID NO: 10: Asp 124 changed to Ser
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC Met Thr Ser Glu Gln Tyr Ser Val.Lys Leu Thr Pro Asp Phe Asp Asn

1	5	10		19	5
	TGG ATT GGA Trp Ile Gly 20				
	AAT GGA AGG Asn Gly Arg 35		ı Met Val T		
	GTT ATA AAC Val Ile Asn				
	GAT GCT GTA Asp Ala Val				
	GAA ACT GAA Glu Thr Glu 85				rg Leu
	GAG GAA TTG Glu Glu Leu 100				
	TGG GGT GAT Trp Gly Asp 115		e Ile Ser I		
	ATT TCA CTG Ile Ser Leu				
	CAA TCG TCA Gln Ser Ser				
	GAA AGT GGA Glu Ser Gly 165	 -	Glu Met T	_	n His
	TTT TGG TAC Phe Trp Tyr 180				
	GTC CCC Val Pro 195				588

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 588 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO

- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE: (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence(B) LOCATION: 1...588(D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity

## (x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO: 11: Glu 135 changed to Ser

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	_		_	Gln	TAC Tyr		_		Leu				_	Asp		48	
1		maa	3 mm	5	COL	010	220	010	10	mmm	3 3 00	mmm	OTT.	15	ama.	0.5	
					CGA Arg											96	
					ATC Ile											144	
					AAT Asn											192	
					GAA Glu 70						•					240	
					TGG Trp											288	
					AAA Lys											336	
					GCA Ala											384	
					GAT Asp											432	
					GAA Glu 150											480	
					CAG Gln											528	
					ACC Thr											576	
	GCT Ala	_														588	



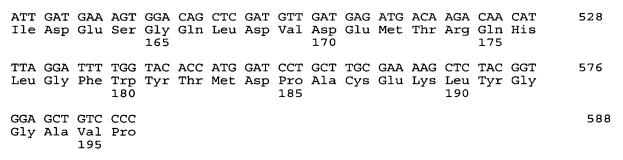


# (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 588 base pairs (B) TYPE: nucleic acid

  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...588
  - (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity
- (x) PUBLICATION INFORMATION: PATENT NO.: 5,360,728
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

 	 	_	_				TTC Phe		48
							CTT Leu 30		96
 			 	_	 	 	AAG Lys		144
							GCC Ala		192
							ATG Met		240
							AAA Lys		288
							ACA Thr 110		336
							GAC Asp		384
							TCT Ser		432
							GTG Val		480

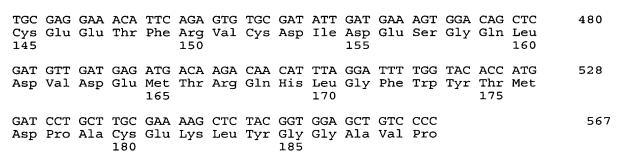


#### (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 567 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: Coding Sequence
  - (B) LOCATION: 1...567
  - (D) OTHER INFORMATION: Recombinant apoaequorin (AQUALITE®)

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

	AAG Lys										48
	CAC His										96
-	GAC Asp	 _	 _	_	 	_		_	_		144
	GCA Ala 50										192
	TTC Phe										240
	TAC Tyr										288
	TCA Ser										336
	GAT Asp										384
	AAA Lys 130									,	432



- (2) INFORMATION FOR SEO ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 236 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x) PUBLICATION INFORMATION: PATENT NO.: 5,484,723
- (ix) FEATURE:
  - (D) OTHER INFORMATION: Vibrio fisheri Flavin reductase
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn 1 5 10 15

Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala 20 25 30

Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe 35 40 45

Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His 50 55 60

Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser 65 70 75 80

Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro 85 90 95

His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu 100 105 110

Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His 115 120 125

Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly 130 135 140

Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala 145 150 155 160

Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu 165 170 175

Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp



Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu
195 200 205

Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys 210 225 220

Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile 225 230 235